

#5

FIG. 1A

Sequence I

-72 AGGAAACCTGCC

-60 ATGGCCTCCTGGTGAGCTGTCTCCTCATCCACTGCTCGCTGCCTCTCCAGATACTCTGACCC

1 M D P L G A A K P Q W P R R C L A A L

1 ATGGATCCCCCTGGGTGCAGCCAAGCCACAATGGCCATGGCGCGCTGTCTGGCCGCACTG

21 L F Q L L V A V C F F S Y L R V S R D D

61 CTATTTCAGCTGCTGGTGGCTGTGTGTTTCTTCTCTACCTGCGTGTGTCCGAGACGAT

41 A T G S P R A P S G S S R Q D T T P T R

121 GCCACTGGATCCCCCTAGGCTCCAGTGGTCCCTCCGACAGGACACCACTCCACCCGC

61 P T L L I L L W T W P F H I P V A L S R

181 CCCACCCTCCTGATCCTGTCTATGGACATGGCCTTCCACATCCCTGTGGCTCTGTCCCGC

81 C S E M V P G T A D C H I T A D R K V Y

241 TGTTCAGAGATGGTGCCCGGCACAGCCGACTGCCACATCACTGCCGACCCGAAGGTGTAC

101 P Q A D T V I V H H W D I M S N P K S R

301 CCACAGGCAGACACGGTCACTCGTGACCACTGGGATATCATGTCCAACCTAAGTCACGC

121 L P P S P R P Q G Q R W I W F N L E P P

361 CTCCCACCTTCCCCGAGGCCCGCAGGGCAGCGCTGGATCTGGTTCAACTGGAGCCACCC

141 P N C Q H L E A L D R Y F N L T M S Y R

421 CCTAACTGCCAGCACCTGGAAGCCCTGACAGATACTTCAATCTCACCATGTCTTACCGC

161 S D S D I F T P Y G W L E P W S G Q P A

481 AGGACTCCGACATCTTACGCCCTACGGCTGGCTGGAGCCGTGGTCCGGCCAGCCTGCCA

181 H P P L N L S A K T E L V A W A V S N W

541 CACCACCGCTCAACCTCTCGGCCAAGACCGAGCTGTGTGGCTGGCGGTGTCCAACCTGG

FIG. 1B

201 K P D S A R V R Y Y Q S L Q A H L K V D  
 601 AAGCGGACTCAGCCAGGTGCGCTACTACCAGAGCCTGCAGGCTCATCTCAAGTGGAC

221 V Y G R S H K P L P K G T M M E T L S R  
 661 GTGTACGGACGCTCCACAAGCCCCCTGCCCAAGGGACCATGATGGAGACGCTGTCCCCG

241 Y K F Y L A F E N S L H P D Y I T E K L  
 721 TACAAGTTCTACCTGGCCTTCGAGAACTCCTTGACCCCGACTACATCACCAGAGAAGCTG

261 W R N A L E A W A V P V L G P S R S N  
 781 TGGAGGAACGCCCTGGAGGCTGGCCGTGCCCGTGGGTGCTGGGCCCCAGCAGAAAGCAAC

281 Y E R F L P P D A F I H V D D F Q S P K  
 841 TACGAGAGGTTCCCTGCCACCCGACGCTTCATCCACGTGGACGACTTCCAGAGCCCCCAAG

301 D L A R Y L Q E L D K D H A R Y L S Y F  
 901 GACCTGGCCCGGTACCTGCAGGAGCTGGACAGGACCACGCCCGCTACCTGAGCTACTTT

321 R W R E T L R P R S F S W A L D F C K A  
 961 CGCTGGCGGAGACGCTGGGCCCTCGCTCCTTCAGCTGGGCACTGGATTCTGCAAGGCC

341 C W K L Q Q E S R Y Q T V R S I A A W F  
 1021 TGCTGGAACCTGCAGCAGGAATCCAGGTACAGACGGTGCGCAGCATAGCGGCTTGGTTTC

361 T \*  
 1081 ACCTGAGAGCCGGCATGGTGCCCTGGGCTGCCGGGAACCTCATCTGCCCTGGGGCCTCACC

1141 TGCTGGAGTCCTTTGTGGCCAAACCTCTCTCTTACTTGGGACCTCACACGCTGGGCTTCA

1201 CGGCTGCCAGGAGCCTCTCCCCCTCCAGAAGACTTGCTGCTAGGGACCTCGCCTGCTGGG

1261 GACCTCGCCTGTGGGACCTCACCTGCTGGGACCTCACCTGCTGGGACCTTGGGCTGC

1321 TGGAGGCTGCACCTACTGAGGATGTGGGGGTCTGGGACTTTACCTGCTGGGACCTGCTC  
 1381 CCAGAGACCTTGCCACACTGAATCTCACCTGCTGGGGACCTCACCCCTGGAGGGCCCTGGG  
 1441 CCCTGGGAACTGGCTTACTTGGGGCCCCACCCGGGAGTGATGGTCTGCGCTGATTGTT  
 1501 TGTGATGTTGTAGCCGCCCTGTGAGGGGTGCAGAGAGATCATCACGGCACGGTTTCCAGA  
 1561 TGTAATACTGCAAGGAAAAATGATGACGTGTCTCCTCACTCTAGAGGGGTGGTCCCCTG  
 1621 GGTTAAGAGCTCACCCACAGGTCTCACCTCAGGGGTTAAGAGCTCAGAGTTCAGACAGGT  
 1681 CCAAGTTCAGCCAGGACCACCACTTATAGGGTACAGGTGGGATCGACTGTAAATGAGG  
 1741 ACTTCTGGAACATTCCAAATATTCTGGGGTTGAGGGGAAATTGCTGCTGTCTACAAAATGC  
 1801 CAAGGGTGGACAGGCGCTGTGGCTCACGCCCTGTAATTCACGACACTTTGGGAGGCTGAGGT  
 1861 AGGAGGATTGATTGAGGCCAACAGTTAAAGACCAGCCTGCTCAATATAGCAAGACCACTG  
 1921 CTCTAAATAAAAAATAATAGGCCGCCAGGAAAAAAAATAAGAAAAA

FIG. 1C

FIG. 2A

Sequence II

-276 CCTTCCCTTGTAGACTCTTCTTGGAATGAGAAAGTAC  
 CGATTCTGCTGAAGACCTCGCGCTCTCAGGCTCTGGAGTTGGAACCCCTGTACCTTCCTT  
 TCCTCTGCTGAGCCCTGCCTCCTTAGGAGGCCAGAGCTCGACAGAACTCGGTTGCTTTG  
 CTGTTTGCTTTGGAGGGAACACAGCTGACGATGAGGCTGACTTTGAACTCAAGAGATCTG  
 CTTACCCAGTCTCCTGGAATTAAGGCTGTACTACATTTGCTGGACCTAAGATTTTC  
 M I T M L Q D L H V N K I S M S R S K S  
 ATGATCACTATGCTTCAAGATCTCCATGTCAACAAGATCTCCATGTCAAGATCCAAGTCA  
 E T S L P S S R S G S Q E K I M N V K G  
 GAAACAAGTCTTCCATCCTCAAGATCTGGATCACAGGAGAAAATAATGATGTCAAGGGA  
 K V I L L M L I V S T V V V V F W E Y V  
 AAAGTAATCCTGTGATGCTGATTGTCTCAACCGTGGTGTGCTGTTTGGGAATATGTC  
 N R I P E V G E N R W Q K D W W F P S W  
 AACAGAATCCAGAGGTTGGTGAGAACAGATGGCAGAGGACTGGTGGTTCCCAAGCTGG  
 F K N G T H S Y Q E D N V E G R R E K G  
 TTTAAAAATGGACCCACAGTTATCAAGAAGACACAGTAGAGGACGGAGAGAAAAGGTT  
 R N G D R I E E P Q L W D W F N P K N R  
 AGAAATGGAGATCGCATTTGAAGAGCCTCAGCTATGGGACTGGTTCAATCCAAAGAACCGC  
 P D V L T V T P W K A P I V W E G T Y D  
 CCGGATGTTTTGACAGTGACCCCGTGGAGGCCCGGATTTGTGTGGAGGCACTTATGAC

FIG. 2B

141	T A L L E K Y Y A T Q K L T V G L T V F
421	ACAGCTCTGCTGGAAGTACTAGCCACACAGAACTCACTGTGGGCTGACAGTGTTT
161	A V G K Y I E H Y L E D F L E S A D M U
481	GCTGTGGAAAGTACATTGAGCATTAAGAGACTTTCTGGAGTCTGCTGACATGTAC
181	F M V G H R V I F Y V M I D D T S R M P
541	TTTCATGGTTGGCCATCGGGTCATATTTACGTCATGATAGACGACACCTCCCGGATGCCT
201	V V H L N P L H S L Q V F E I R S E K R
601	GTCGTGCACCTGAACCTCTACATTCCTTACAAGTCTTTGAGATCAGGTCTGAGAAAGAGG
221	W Q D I S M M R M K T I G E H I L A H I
661	TGGCAGGATATCAGCATGATGGCATGAAGACCATTGGGGAGCACATCTGGCCACATC
241	Q H E V D F L F C M D V D Q V F Q D N F
721	CAGCAGAGGTCGACTTCTCTTCTGTCATGGACGTGGATCAAGTCTTTCAAGACAACCTC
261	G V E T L G Q L V A Q L Q A W W Y K A S
781	GGGGTGGAAACTCTGGCCAGCTGGTAGCACAGCTCCAGGCCCTGGTGTACAAAGCCAGT
281	P E K F T Y E R R E L S A A Y I P F G E
841	CCCGAGAAAGTTCACCTATGAGAGCGGGAAGTGTGGCCGCGGTACATTCATTCCGGAGAG
301	G D F Y Y H A A I F G G T P T H I L N L
901	GGGGATTTTACTACACCGCGCCATTTTGGAGGAACGCTACTCACATTCTCAACCTC
321	T R E C F K G I L Q D K K H D I E A Q W
961	ACCAGGGAGTGCTTAAGGGGATCCTCCAGGACAAGAAACATGACATAGAAGCCAGTGG
341	H D E S H L N K Y F L F N K P T K I L S
1021	CATGATGAGGCCACCTCAACAAATACTTCTCTTTCAACAAACCCACTAAATCCTATCT

361 P E Y C W D Y Q I G L P S D I K S V K V  
1081 CCAGAGTATTGCTGGGACTATCAGATAGGCCTGCCCTTCAGATATTAAAAGTGTCAAGGTA  
381 A W Q T K E Y N L V R N N V \*  
1141 GCTTGGCAGACAAAGAGTATAATTGGTTAGAAATAATGTCTGACTTCAAATTTGTGATG  
1201 GAAACTTGACACTATTCTTAACCA

FIG. 2C

Sequence III

10	20	30	40	50	60
GAATTCATCGTGGCAAGGCAGCCTGAATGGATGATGTAACTGGGGTCTTTCAATGG					
70	80	90	100	110	120
AGGGCCAGACTCCTGGGTCTAGGGGATGAGGAGGGAGGATCGGGTAGCTGGGACCCA					
130	140	150	160	170	180
GGTGAAAGGGGCTGGGGCCACATTCCTGAGTCTCAGAGAGAAGGATCTGGGGTCTCAA					
190	200	210	220	230	240
GCACCTGAGTCGGAGGGAGGGGTGCTGGGCTCCTGGAAACCACCTCTTGGACCAT					
250	260	270	280	290	300
CTATGCAGATCAGCAGAACCAAGAGAAATTTCTGCGCCCCATCTGAATTTCTAAGTTTGG					
310	320	330	340	350	360
GGGAGGGCGTGATCTGACACTGAGGTTCTTGTATCCTCAGCAAGGCGCAATTGCTGTA					
370	380	390	400	410	420
TGAAAGAAGCGACCGCATCTGAGACACAAGTATCCTGCCTTGAAGCCTCTCACCTGGCC					
430	440	450	460	470	480
GTGGGCCAACCTCAACCTCATCTGTCCCTGCTCAGATGCTCAGACCCCTGGACATCCCAGC					
490	500	510	520	530	540
CTCCCTCCTGATGCAATCCTGGTGTCTTTTCCACAGAGAAGCCATCCCAGGCCCAG					
550	560	570	580	590	600
GCAGGTGCTCCTGAAATAACCTGGGGGAGGGGTGGCTGAAAGTCCCTGACTGGAGTTGG					
610	620	630	640	650	660
CAGCCAAGCCAGGCCCTGGAGTGGGCGCACCAGAGGGAAGACAGGTTGGCTAATTTCCCTGG					

FIG. 3A

FIG. 3B

670	680	690	700	710	720
AGCCCCTAAGGGTGCAAGGGTAGGCCCTTCTGTGTCTGAGGGAGGAGGGCTGGGGCTCTGG					
730	740	750	760	770	780
ACTCCTGGGTCTGAGGGAGGAGGGGTGGGGGCCCTGGACTCCTGGTCTGAGGGAGGAGG					
790	800	810	820	830	840
GTCTGGGCCTGTACTCCTGGATCTGAGGGAGGAGGGCTGGGAACTTGGGCTCCTGGGT					
850	860	870	880	890	900
CTGAGGAGGAGGAGCTTTGGTCTGGACTCCTGGGTCTGAGGGAGTAGGGCTAGGGAT					
910	920	930	940	950	960
CTGGACTCGTGGGTGTGAGGAAGGAGGGCTGGGTCTGGACTCCTGGTCTGAGGAAG					
970	980	990	1000	1010	1020
GAGGGCAGGGGCTTGGACTCCTGGTCTGAGGAAGGAGGGCCGGAGCCTGGACTCC					
1030	1040	1050	1060	1070	1080
TAAGTCTGAGGGAGGAGGTCTGGGGCCTGGACTGTGGTGTGAGCACAAAGGCTCTGG					
1090	1100	1110	1120	1130	1140
GTGCTGGGAGTCCCAGCCTGGGAGATGATGGTTAACTTCTGGGAATCAAGTCAAAC					
1150	1160	1170	1180	1190	1200
CCTGAGTCTTTGACATTGATGTATCTTGAATGGAGGTCAGTCTGTGGGAAGGATTAC					
1210	1220	1230	1240	1250	1260
CCAGGTCCGAGGCAAGAGACTGAAGGCACAACTGTTTCAGTATAATAAGAAAAATAGT					
1270	1280	1290	1300	1310	1320
TAGAATAAGAAATAGTTATCATACAAATTAGATATAGAGATGATCATGGACAGTATCAATC					



1330 1340 1350 1360 1370 1380  
 ATTAGTAAACATTATTAATCATTAGCTATTACTTTTATTCTTTGTTGATAACTAATA  
 1390 1400 1410 1420 1430 1440  
 TAACCAGGAAACAACCGGTGGTATAGGTCAGGTACTGAAGGGACATTGTGAGAAGTGA  
 1450 1460 1470 1480 1490 1500  
 CCTAGAAGGCAAGAGGTGAGCCTTCTGTCAACCGGCATAAGGGCCTCTTGAGGGCTCCT  
 1510 1520 1530 1540 1550 1560  
 TGGTCAAGGGGAACGCCAGTGTCTGGGAAGGCACCCGTTACTCAGCAGACCACGAAAGG  
 1570 1580 1590 1600 1610 1620  
 GAATCTCCTTTTCTTGGAGGAGTCAGGGAACACTCTGCTCCACCAGCTTCTTGTGGGAGG  
 1630 1640 1650 1660 1670 1680  
 CTGGGTATTATCTAGGCCCTGCCCGCAGTCATCCTGCTGTGCTGTGCTTCAATGGTCACGC  
 1690 1700 1710 1720 1730 1740  
 TCCTTGTCCTCTTGCAATTTTCCTCCCGTACTCCTGGTTCCCTCTTTGAAGTTCGTAGTAGA  
 1750 1760 1770 1780 1790 1800  
 TAGCGGTAGAAAGAAATAGTGAAAGCCTTTTCTTTTCTTTTGTAGGCGGAGTCTCGCTC  
 1810 1820 1830 1840 1850 1860  
 TGTCCCCCAGGCTGGAGTGCAGTGGCGTGATCTCGGCTCACTGCAATCTCCGCCCTCCTGG  
 1870 1880 1890 1900 1910 1920  
 GTTCACACCATTCCTCTGCCTCACCTCCCAAATAGCTAGGACTACAGGCGCCCTCCACC  
 1930 1940 1950 1960 1970 1980  
 ACGGCCCCGGATAATTTTGTATTTTAGTAGAGACAGGGTTTCAACCGTGTAGCCAGG

FIG. 3C

# FIG. 3D

1990	2000	2010	2020	2030	2040
ATGGCCTCCACCTCCTGACCTTGATCCGCCCGCTCAGCCTCCCAAAGTCTGGGATT					
2050	2060	2070	2080	2090	2100
ACAGGCGTGAGCCACCGCGCCCGCCGAAATAGTAAAGTCTTAAAGTCTTTGATCTTTC					
2110	2120	2130	2140	2150	2160
TTATAAGTGCAGAGAAAGAAACGCTGACATATGCTGCTTCTCTTCTGCTTCGGCTGCC					
2170	2180	2190	2200	2210	2220
TAAAGGGAAGGCCCCCTGTCCCATGATCACGTGACTTGCTTGACCTTATCAGTCATTT					
2230	2240	2250	2260	2270	2280
GGACGACTCACCTCCTTATCCTGCTGCCCCCTTGCTTGATACAAATAATATCAGCGCG					
2290	2300	2310	2320	2330	2340
CCCAGCCATTGGGGCCACTACCGGTCTCTGCGTCTTGATGGTAGTGGTCCCCCGGCC					
2350	2360	2370	2380	2390	2400
AGCTGTTTTCTCTTATCTCTTTGTCTTGCTCTTATTTCTTACAATCTCTCCTCTCCT					
2410	2420	2430	2440	2450	2460
CACAGGGAAGAAACACCCACCCGCAAGCCCCGTAGGGCTGGACCCCTACGTTAGCCTGCC					
2470	2480	2490	2500	2510	2520
CTGCTCGGGTTGGCGATGCTGGAGGTGGGCTTGACCCAGAGAAAATGCTTAAATTAGG					
2530	2540	2550	2560	2570	2580
TGACAAGCGGCGAGAGCCCTTGTCTCTGGCGCGGACCCACGCGCCCCCGCTGACGGCG					
2590	2600	2610	2620	2630	2640
TGGGAAACAGACCCCTGTTCCACTCCGGTCTCCAGCCTTGAATGGTTGCCCTTCGTGCAGT					

FIG. 3E

2650	2660	2670	2680	2690	2700
GCAGGCTGGAAAGTAGCAGTTTGGCAGGGACCCCTAGAAATCCCCAAAGGAGTGACTA					
2710	2720	2730	2740	2750	2760
GGGGCTGGGATTCTGGAAATTGAGTGTGACGGTGAGCGGGGGGTGTGGGAGATCGGAG					
2770	2780	2790	2800	2810	2820
ACCCTGTGGCGCGGAGACACCTGCAGGCTGGAGGCCCTCGCGCGCTCCGGCGGACGCC					
2830	2840	2850	2860	2870	2880
TGGCAAACAGGTTCTCCATCCCCCAGGAGGACCGCGGACAGGGCGGACGATCGCTCCACT					
2890	2900	2910	2920	2930	2940
CGCCGGACACAGGTGCGGGGGCCCTGCCAGCCGCTGGGCGTGCGGCGGCTCGAAGCAC					
2950	2960	2970	2980	2990	3000
CCAGGTGTCGGGGCCGACTCTAAGCCCTGGCACCCGGAAGAGAGAGGGCGGGGATTGGA					
3010	3020	3030	3040	3050	3060
CCTCCCGGCTCCAGCATTGCAACTGGGCGCTCCGTCTCCTGTCCACGCAATGATGCTGC					
3070	3080	3090	3100	3110	3120
GGCTGCTCAGAAAGCCAGGTAGCCTGCCCTGGGTGAAGCCTTCGCGCAGGTCAATGACGGG					
3130	3140	3150	3160	3170	3180
GCGGAGGGCAGGGCGCGGTCCCCTGCATCCCCGATCTGGGGAGCGGTGGGCCACGGGC					
3190	3200	3210	3220	3230	3240
CATCGCCTTAGCCCCCTGGCGCTGGGGCTCGGGCGCAAGTACGGGGCGGGCTCCACCTTC					
3250	3260	3270	3280	3290	3300
CAGCCATCCGCCCGCCGGAGGGCGGACGCTGCGAGACTCCCGCGCGGCCCTCTCCT					

FIG. 3F

3310	3320	3330	3340	3350	3360
TCCTCTCTCCCAAGCCCTCGCTGCCAGTCCGGACAGGCTGCGGAGGGAGGGCTGC					
3370	3380	3390	3400	3410	3420
CGGGCCGGATAGCCGGACGCCCTGGCGTTCCAGGGGCGCGCGGATGTGGCCTTTCCTTTCG					
3430	3440	3450	3460	3470	3480
GAGGGTGGCTCCGGCCACGAAAGCGGACTGTGGATCTGCCACCTGCAAGCAGCTCGGC					
3490	3500	3510	3520	3530	3540
TAAGTGGGACTGCCCCACTCACTAGTTGTTCTCTGGGACCCAGGAACAACCTTCAGAACCA					
3550	3560	3570	3580	3590	3600
GGAGGTGACCCCAACCTCTTCTCCAGGTCTTCTTAAGGCCCTAGGAATCTCCGCCACC					
3610	3620	3630	3640	3650	3660
TCCCCAGCCATTACTCTCCAGGAACCAAGATGCTCTTCCGCTCTGACCCCTCCAGCCT					
3670	3680	3690	3700	3710	3720
CTCTTGTTTACTTGAACATATCGTTTCCCATCACCACTCTGTGGTGATTTTGGCCTC					
3730	3740	3750	3760	3770	3780
ACAGACAGGTACTCCTGAGAAACAGGCTGGTGAAGAGTCCAGTATCAGCGGAACCTTASC					
3790	3800	3810	3820	3830	3840
AGGAGGGGAGACTCGAGATTCTTTCAGGAAAGGTGTAGGAACCTGGACCACTTCTTTT					
3850	3860	3870	3880	3890	3900
TTTTTTTTTTTTTTTAAAGACAGGGTCCCTCTCTGTCCGGCAAGCTGGAGTGCAGTCAG					
3910	3920	3930	3940	3950	3960
CGGTGCTATCGGGCTCATTTGTGAGCTCCGGGGATCCTCCCGCCTTAGCATCCGGTGTAG					

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FIG. 36

3970 3980 3990 4000 4010 4020  
CTGAGACCACAGACATGTGCCACCATGCCAAGCTAATTTATTTATTTTGGAGAC  
4030 4040 4050 4060 4070 4080  
GGAGTTTCACTCTTGTGCCAGGCTGGAGTGTAATGGCATGATCTCAGCTCACCGCAAC  
4090 4100 4110 4120 4130 4140  
TCCCGCCCCGGGTTCAGGCGATTCTCCTGCCTCAGCCTCCCGAGTGGCTGGGATTACA  
4150 4160 4170 4180 4190 4200  
GGCATGCGCCACCATGCCCGGCTAATTTGTATTTTAAGTAGAGACAGGGTTTCTCCACG  
4210 4220 4230 4240 4250 4260  
TTGGTCAGGCTGGTCTCGAACTCCCAACCTCAGGTGATCCACCCACCTTGGCCTCCCAA  
4270 4280 4290 4300 4310 4320  
GTGCTGGGATTACAGGTGTGAGCCACCGCGCTGGCCCATGCCAAGCTAATTTTAAATT  
4330 4340 4350 4360 4370 4380  
TTTTTGAAGAGTGCTCTGTTGCCAGGCTGATCTTGAACCTCTGGGCTCAAGGGATCCT  
4390 4400 4410 4420 4430 4440  
CCCATCTCAGCCTCCCAATATGCTGGGATTACAGGTGTGAGCCACAGTGCCAGCCAAAC  
4450 4460 4470 4480 4490 4500  
CATGGCTATCTTGAAAACCACTTGTCTTCCAGTCCCCCATGCCCGAAATTCCAAGGCTCT  
4510 4520 4530 4540 4550 4560  
CATCCCTGAACCTAGGACTCAGGCTCTCCCTACCTCAGCCCCCAGGAGTCTAAACCTTA  
4570 4580 4590 4600 4610 4620  
ACTTCCCTCTTTCCCTGGGACTAAGAGGTGCTGCACCCAGGGCCTCCCTTACCCACAT

FIG. 3H

4630	4640	4650	4660	4670	4680
CCCTCCTCAGCCTCCCTCCTCAGCCTCAGTGCAATTGCTAATTCGCCTTCTCCTCCCTG					
4690	4700	4710	4720	4730	4740
CAGCCATGTGGCTCGGAGCCATCGTCAGCTCTGCCTGGCCTTCTGCTAGTGTGTCC					
MetTrpLeuArgSerHisArgGlnLeuCysLeuAlaPheLeuLeuValCysVal					
4750	4760	4770	4780	4790	4800
TCTCTGTAATCTTCTCCTCCATATCCATCAAGACAGCTTTCACATGGCCTAGGCCTGT					
euSerValIlePhePheLeuHisIleHisGlnAspSerPheProHisGlyLeuGlyLeus					
4810	4820	4830	4840	4850	4860
CGATCCTGTGTCCAGACCGCGCCTGTGTGACACCCCGAGTGGCCATCTTCTGCCTGCCGG					
erIleLeuCysProAspArgArgLeuValThrProProValAlaIlePheCysLeuProG					
4870	4880	4890	4900	4910	4920
GTA CTGGATGGCCCCAACGCTCCTCTCTCCTGTCCCGACACCTGCTTCCCTCTCCG					
lyThrAlaMetGlyProAsnAlaSerSerSerCysProGlnHisProAlaSerLeuSerG					
4930	4940	4950	4960	4970	4980
GCACCTGGACTGTCTACCCCAATGGCCGTTTGGTAATCAGATGGGACAGTATGCCACGC					
lyThrTrpThrValTyProAsnGlyArgPheGlyAsnGlnMetGlyGlnTyAlaThrL					
4990	5000	5010	5020	5030	5040
TGCTGGCTCTGGCCAGCTCAACGGCCGCGGCTTTATCCTGCTGCCATGCATGCCG					
euLeuAlaLeuAlaGlnLeuAsnGlyArgArgAlaPheIleLeuProAlaMetHisAlaA					
5050	5060	5070	5080	5090	5100
CCCTGGCCCCGGTATTCGCGCATCACCTGCCCCGTGCTGGCCCCAGAGTGACAGCCGCA					
laLeuAlaProValPheArgIleThrLeuProValLeuAlaProGluValAspSerArgT					
5110	5120	5130	5140	5150	5160
CGCCGTGGCGGAGCTGCAGCTTCACGACTGGATGTCGGAGGAGTACGGGACTTGAGAG					
hrProTrpArgGluLeuGlnLeuHisAspTrpMetSerGluGluTyAlaAspLeuArgA					

5170 5180 5190 5200 5210 5220  
 ATCCTTCTGAAGCTCTCTGGCTTCCCCTGCTCTTGACTTTCTCCACCATCTCCGGG  
 spPropheLeuLysLeuSerGlyPheProCysSerTrpThrPhePheHisHisLeuArgG  
 5230 5240 5250 5260 5270 5280  
 AACAGATCCGCAGAGATTACCCCTGCACGACACCTTCGGGAAGAGCGCAGAGTGTGC  
 luGlnIleArgArgGluPheThrLeuHisAspHisLeuArgGluGluAlaGlnSerValL  
 5290 5300 5310 5320 5330 5340  
 TGGGTACGCTCCGCCCTGGCCGCACAGGGGACCGCCCGCCGACCTTTGTCTGGCGTCCACG  
 euGlyGlnLeuArgLeuGlyArgThrGlyAspArgProArgThrPheValGlyValHisV  
 5350 5360 5370 5380 5390 5400  
 TCGCGCCGTGGGACTATCTGCAGGTTATGCCCTCAGCGCTGGAAGGTGTGTGGCGGACA  
 alArgArgGlyAspTyrLeuGlnValMetProGlnArgTrpLysGlyValValGlyAsps  
 5410 5420 5430 5440 5450 5460  
 GCGCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCCGTTTCG  
 erAlaTyrLeuArgGlnAlaMetAspTrpPheArgAlaArgHisGluAlaProValPheV  
 5470 5480 5490 5500 5510 5520  
 TGGTCACCAGCAACGGCATGGAGTGGTGTAAAGAAACATCGACACCTCCCGAGGCGATG  
 alValThrSerAsnGlyMetGluTrpCysLysGluAsnIleAspThrSerGlnGlyAspV  
 5530 5540 5550 5560 5570 5580  
 TGACGTTTGCTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCACAC  
 alThrPheAlaGlyAspGlyGlnGluAlaThrProTrpLysAspPheAlaLeuLeuThrg

FIG. 31

5590 5600 5610 5620 5630 5640  
AGTGCAACACACATTATGACCATTTGGCACCTTCGGCTTCTGGGCTGCCTACCTGGCTG  
InCysAsnHisThrIleMetThrIleGlyThrPheGlyPheTrpAlaAlaTyrLeuAlaG  
5650 5660 5670 5680 5690 5700  
GCGGAGACACTGTCTACCTGGCCAACTTCACCCCTGCCAGACTCTGAGTTCCTGAAGATCT  
lyGlyAspThrValTyrLeuAlaAsnPheThrLeuProAspSerGluPheLeuLysIleP  
5710 5720 5730 5740 5750 5760  
TTAAGCCGGAGGGCCCTTCCTGCCAGTGGTGGGCATTAATGCAGACTTGTCTCCAC  
heLysProGluAlaAlaPheLeuProGluTrpValGlyLeuAsnAlaAspLeuSerProL  
5770 5780 5790 5800 5810 5820  
TCTGGACATTGGCTAAGCCTTGAGAGCCAGGGAGACTTTCCTGAAGTAGCCTGATCTTCT  
euTrpThrLeuAlaLysProEnd  
5830 5840 5850 5860 5870 5880  
AGAGCCAGCAGTACGTGGCTTCAGAGGCCCTGGCATCTTCTGGAGAAAGCTTGTGTGTTC  
5890 5900 5910 5920 5930 5940  
TGAAGCAAAATGGGTGCCCGTATCCAGAGTGATTCTAGTTGGGAGAGTTGGAGAGAAGGGG  
5950 5960 5970 5980 5990 6000  
GACGTTCTGGAAGTGTCTGAATATTCTAGAACTAGCAAAACATCTTTTCTGATGGCTG  
6010 6020 6030 6040 6050 6060  
GCAGGCAGTTCTAGAAGCCACAGTGCCCACTGCTCTTCCAGCCCATATCTACAGTACT  
6070 6080 6090 6100 6110 6120  
TCCAGATGGCTGCCCCCAGGAATGGGAACTCTCCCTCTGGTCTACTCTAGAAGAGGGGT  
6130 6140 6150 6160 6170 6180  
TACTTCTCCCTGGGTCTCCAAAGACTGAAGGAGCATATGATTGTCTCCAGAGCAAGCAT

FIG. 3J



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FIG. 3K

FIG. 3L

6850 6860 6870 6880 6890 6900  
 AGAGACGGGGTTTCATCGTGTAAACCAGGATGGTCTCGATCTCCTGACCTCGTGATCTGC  
 6910 6920 6930 6940 6950 6960  
 CCACCTCGGCCTCCACAGTGTCTGGGATTACCGGCGTGAGCCACCATGCCTGGCCCGGAT  
 6970 6980 6990 7000 7010 7020  
 AATTTTTTTTAAATTTTGTAGAGACGAGGTCTTGTGATATTGCCCAGGCTGTTCTTCAAC  
 7030 7040 7050 7060 7070 7080  
 TCCTGGGCTCAAGCAGTCCTCCACCTTGGCCTCCAGAAATGCTGGGTTTATAGATGTGA  
 7090 7100 7110 7120 7130 7140  
 GCCAGCACACCGGGCCAAGTGAAGAATCTAATGAATGTGCAACCTAATTGTAGCATCTAA  
 7150 7160 7170 7180 7190 7200  
 TGAATGTTCCACCATTGCTGGAAAAATTGAGATGGAAAAACCAACCATCTCTAGTTGGCCA  
 7210 7220 7230 7240 7250 7260  
 GCGTCTTGCTCTGTTACAGTCTCTGGAAAAGCTGGGGTAGTTGGTGAGCAGAGCGGGAC  
 7270 7280 7290 7300 7310 7320  
 TGTGTCCAACAAGCCCCACAGCCCCCTCAAGACTTTTTTTTGTGTTTGTGAGCAGACAG  
 7330 7340 7350 7360 7370 7380  
 GCTAAATGTGAACGTGGGTGAGGATCACTGCCAAAATGGTACAGCTTCTGGAGCAGA  
 7390 7400 7410 7420 7430 7440  
 ACTTTCAGGGATCCAGGGACACTTTTTTTTAAAGCTCATAAACTGCCAAGAGCTCCATA  
 7450 7460 7470 7480 7490 7500  
 TATTGGGTGAGTTCAGGTGCGCTCTCACAAATGAAGGAAGTTGGTCTTTGTCTGCAGGT

7510 7520 7530 7540 7550 7560  
 GGGCTGCTGAGGGTCTGGGATCTGTTTCTGGAAGTGCAGGTATAAACACACACCCCTCTG

7570 7580 7590 7600 7610 7620  
 TGCTGTGACAAACTGGCAGGTACCGTGTCTCATTTGCTAACCACTGTCTGTCCCTGAACCTC

7630 7640 7650 7660 7670 7680  
 CCAGAACCACTACATCTGGCTTTGGGCAGGTCTGAGATAAAACGATCTAAAGGTAGGCAG

7690 7700 7710 7720 7730 7740  
 ACCCTGGACCCAGCCCTCAGATCCAGGCAGGACGAGGTCTGGCCAAAGTGGACGGGGT

7750 7760 7770 7780 7790 7800  
 TGTCGAGATCTCAGGAGCCCCCTTGCTGTTTTTTGGAGGGTGAAAGAAACCTTAAACA

7810 7820 7830 7840 7850 7860  
 TAGTCAGCTCTGATCACAATCCCCCTGTCTACTCATCCAGACCCCATGCCTGTAGGCTTATC

7870 7880 7890 7900 7910 7920  
 AGGGAGTTACAGTTACAATTGTTACAGTACTGTTCCTCACTCAGCTGCCACGGGTGAGAG

7930 7940 7950 7960 7970 7980  
 AGCAGGAGGTATGAATTAAAGTCTACAGCACATAACCCGTGTCTCTGTAGCTTTTTTGGGA

7990 8000 8010 8020 8030 8040  
 GCCAGAGCCCACTGTGTATGTGTGTGGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT

8050 8060 8070 8080 8090 8100  
 AAGAGAGTGGAGGAAAAGGTGGGGTACTTCTGAAGACTTTTATTTTTTTTTTAATTAATTT

8110 8120 8130 8140 8150 8160  
 ATTTTTTTCAGAGATCGAGTCTTGCTCTGTGGCCCAAGCTGGAGTGCAGTAGTGTGATC

FIG. 3M

FIG. 3N

8170  
TCGGCCCACTGCAA

FIG. 3N

10	*	20	*	30	*	40	*	50	*	60	*
CTGCA	GAGAG	CGCCA	CCCGG	AAGCC	ACTTT	TATAG	AAGCT	TTTAC	ACACA	ATGCT	TGATT
70	*	80	*	90	*	100	*	110	*	120	*
TTTTT	TTTTT	TTTTC	CGAGA	CGGAG	TCCTCG	CTTTG	TCGCC	CAGGC	TGGAG	TGCAG	TGGCG
130	*	140	*	150	*	160	*	170	*	180	*
CGATC	TGGGC	TCACT	GCAAG	CTCCG	CCTCC	TGGGT	TGACG	CCATT	CTCCT	GCCTC	AGCTT
190	*	200	*	210	*	220	*	230	*	240	*
CCCCA	GTAGC	TGGGA	CTACA	GGCGC	CCGCC	ACCAA	GCCTG	GCTAA	TTTTT	TTTTA	TTTTT
250	*	260	*	270	*	280	*	290	*	300	*
AGTGG	AGACA	GAGTT	TCACC	GTGTT	AGCCA	GGATG	GTCTC	GATCT	CCTGA	CCTCG	GGATC
310	*	320	*	330	*	340	*	350	*	360	*
CGCCC	GCCTC	GGCCT	CCCAA	AGTGC	TGGGA	GTATA	GGCGT	GAGCC	ACCGC	GCCTG	GCCTA
370	*	380	*	390	*	400	*	410	*	420	*
TACTT	GATTT	TTAAT	GAAAA	CATTC	TTAAA	TTTAT	ATGGC	TAACG	CAAAAT	TTATT	TTCTG
430	*	440	*	450	*	460	*	470	*	480	*
TAGGC	ATAAC	ATCAA	AAACA	CCTGG	CAGGA	CTGCC	CCATT	CCCAG	CACCTG	TCTAG	TTCTC

FIG. 4A

SEQUENCE SHEET

490	*	500	*	510	*	520	*	530	*	540	*
CCCTA	GTATC	AGTGG	GACTC	CACTG	ATGCA	CAGCT	GTGAT	CTACT	AAAAC	TTCTC	TCAAA
550	*	560	*	570	*	580	*	590	*	600	*
ACTTT	CTCCT	TAGGT	CAGCA	GCCCC	GGCCC	TGATC	TATTT	GGAAA	TCCCC	TGAAT	
610	*	620	*	630	*	640	*	650	*	660	*
AAAAG	TTGAA	TATCA	TAAAC	CAAAG	CGAAC	ACCCA	GAAAT	TCAAA	TTCAA	CCCCG	AGGTA
670	*	680	*	690	*	700	*	710	*	720	*
AAAAA	TTTCT	CAAGT	GACTG	TAGAC	GTAGA	TGTCT	CCAGT	GTCGC	CTAAT	AAGGT	AGAAG
730	*	740	*	750	*	760	*	770	*	780	*
AGGCC	AGTGC	GATAC	TGTCT	TTACA	CCCTT	AACCT	GGGTG	CTAGA	ATATT	TATCT	TCGTC
790	*	800	*	810	*	820	*	830	*	840	*
ATCAT	TTTAT	CATCC	AAACT	ATTTT	GCATA	ACTTT	CATGG	GTGCA	GAAAA	TGTTT	TTTAA
850	*	860	*	870	*	880	*	890	*	900	*
GTGCT	TGGTA	AAATT	AATAG	TGATA	TTCAT	TCATT	CATCT	CACTG	AACAG	GCAAT	AAATT
910	*	920	*	930	*	940	*	950	*	960	*
CCTTG	ACGAC	AAGGG	CCTTG	GGGGG	GGCCA	CATCT	TCATC	TTTGG	TTTAT	GAGTC	CTGTG

FIG. 4B

970 *	980 *	990 *	1000 *	1010 *	1020 *
CGTCT TGGTA	CAAGC AATAC TACTA TGAGC CGGCA AGTCA GACTT ATTTG GTAGG GGACC				
1030 *	1040 *	1050 *	1060 *	1070 *	1080 *
AAAGG AAAGA ACATG TTTTG ATTGC TAAGA AAACA TTTTG TTCTC TATTC TTTAC TGGGC					
1090 *	1100 *	1110 *	1120 *	1130 *	1140 *
TGGCA GGCAA AGGAA ATGTT CTTAT GAGCA CTCAC ATTGA AAACCT TAAGT TCTTC ACCAA					
1150 *	1160 *	1170 *	1180 *	1190 *	1200 *
ATGCA GAGAC TCTGA AGGCC ACGCC GCTGC GGGCT GCCTC CACAA TTCGA CCGTC TCGGC					
1210 *	1220 *	1230 *	1240 *	1250 *	1260 *
GGGCC ACGAG ATCCT GGCCA CGGAT GCGGT GGCCG CGCCT CTGCT CGCAC GTTCC CCCGG					
1270 *	1280 *	1290 *	1300 *	1310 *	1320 *
CCTCT GGACT CCCTC CCTCC CTCAA TCCCT CCCTC CGGCG GGCCT CGCTG GCGGG TGGCT					
1330 *	1340 *	1350 *	1360 *	1370 *	1380 *
AGGCC CAACG GCAGG AAGCC GACGC TATCC TCCGT TCCGC GCGGC CCGGT CCGCC TTCCG					
1390 *	1400 *	1410 *	1420 *	1430 *	1440 *
TCTGT TCTAG GGCCT GCTCC TGCGC GGCAG CTGCT TTAGA AGGTC TCGAG CCTCC TGTAC					

FIG. 4C

FIGURE 38

1450 *	1460 *	1470 *	1480 *	1490 *	1500 *
CTTCC CAGGG ATGAA CCGGG CCTTC CCTCT GGAAG GCGAG GGTTC GGGCC ACAGT GAGCG					
1510 *	1520 *	1530 *	1540 *	1550 *	1560 *
AGGGC CAGGG CCGTG GCGGC GCGCA GAGGG AAACC GGATC AGTTG AGAGA GAATC AAGAG					
1570 *	1580 *	1590 *	1600 *	1610 *	1620 *
TAGCG GATGA GCGCG TTGTG GGGCG CCGCC CGGAA GCCCT CCGGC GCGGC CTGGG AGAAG					
1630 *	1640 *	1650 *	1660 *	1670 *	1680 *
GAGTG GCGCG AGGCG CCGCA GGAGG CTCCC CGGGC CTGGT CCGGC CCGCT GGGCC CCGGG					
1690 *	1700 *	1710 *	1720 *	1730 *	1740 *
CGCAG TGGAA GAAAG GGACG GGCGG TGCCC GGTG GCGGT CCTGG CCAGC TCACC TTGCC					
1750 *	1760 *	1770 *	1780 *	1790 *	1800 *
CTGGC GGCTC GCCCC GCCCC GCACT TGGGA GGAGC AGGGC CCGCG GCCTT TGCAT					
1810 *	1820 *	1830 *	1840 *	1850 *	1860 *
TCTGG GACCG CCCCC TTCCA TTCCC GGGCC AGCGG CGAGC GGCAG GCTGG AGCCG					
1870 *	1880 *	1890 *	1900 *	1910 *	1920 *
CAGCT ACAGC ATGAG AGCCG GTGCC GCTCC TCCAC GCCTG CCGAC GCGTG GCGAG CCGAG					

FIG. 4D



FIG. 4E

1930	1940	1950	1960	1970
* GCAGC GCTGC CTGTT CGCGC C ATG GGG GCA CCG TGG GGC TCG CCG ACG GCG GCG Met Gly Ala Pro Trp Gly Ser Pro Thr Ala Ala	* GCAGC GCTGC CTGTT CGCGC C ATG GGG GCA CCG TGG GGC TCG CCG ACG GCG GCG	* GCAGC GCTGC CTGTT CGCGC C ATG GGG GCA CCG TGG GGC TCG CCG ACG GCG GCG	* GCAGC GCTGC CTGTT CGCGC C ATG GGG GCA CCG TGG GGC TCG CCG ACG GCG GCG	* GCAGC GCTGC CTGTT CGCGC C ATG GGG GCA CCG TGG GGC TCG CCG ACG GCG GCG
1980	1990	2000	2010	2020
* GCG GGC GGG CGG CGC GGC TGG CGC CGA GGC GGC GGC CTG CCA TGG ACC GTC TGT Ala Gly Gly Arg Arg Gly Trp Arg Arg Gly Arg Gly Leu Pro Trp Thr Val Cys	* GCG GGC GGG CGG CGC GGC TGG CGC CGA GGC GGC GGC CTG CCA TGG ACC GTC TGT Ala Gly Gly Arg Arg Gly Trp Arg Arg Gly Arg Gly Leu Pro Trp Thr Val Cys	* GCG GGC GGG CGG CGC GGC TGG CGC CGA GGC GGC GGC CTG CCA TGG ACC GTC TGT Ala Gly Gly Arg Arg Gly Trp Arg Arg Gly Arg Gly Leu Pro Trp Thr Val Cys	* GCG GGC GGG CGG CGC GGC TGG CGC CGA GGC GGC GGC CTG CCA TGG ACC GTC TGT Ala Gly Gly Arg Arg Gly Trp Arg Arg Gly Arg Gly Leu Pro Trp Thr Val Cys	* GCG GGC GGG CGG CGC GGC TGG CGC CGA GGC GGC GGC CTG CCA TGG ACC GTC TGT Ala Gly Gly Arg Arg Gly Trp Arg Arg Gly Arg Gly Leu Pro Trp Thr Val Cys
2030	2040	2050	2060	2070
* GTG CTG GCG GCC GCG GGC TTG ACG TGT ACG GCG CTG ATC ACC TAC GCT TGC TGG Val Leu Ala Ala Ala Gly Leu Thr Cys Thr Ala Leu Ile Thr Tyr Ala Cys Trp	* GTG CTG GCG GCC GCG GGC TTG ACG TGT ACG GCG CTG ATC ACC TAC GCT TGC TGG Val Leu Ala Ala Ala Gly Leu Thr Cys Thr Ala Leu Ile Thr Tyr Ala Cys Trp	* GTG CTG GCG GCC GCG GGC TTG ACG TGT ACG GCG CTG ATC ACC TAC GCT TGC TGG Val Leu Ala Ala Ala Gly Leu Thr Cys Thr Ala Leu Ile Thr Tyr Ala Cys Trp	* GTG CTG GCG GCC GCG GGC TTG ACG TGT ACG GCG CTG ATC ACC TAC GCT TGC TGG Val Leu Ala Ala Ala Gly Leu Thr Cys Thr Ala Leu Ile Thr Tyr Ala Cys Trp	* GTG CTG GCG GCC GCG GGC TTG ACG TGT ACG GCG CTG ATC ACC TAC GCT TGC TGG Val Leu Ala Ala Ala Gly Leu Thr Cys Thr Ala Leu Ile Thr Tyr Ala Cys Trp
2090	2100	2110	2120	2130
* GGG CAG CTG CCG CCG CTG CCC TGG GCG TCG CCA ACC CCG TCG CGA CCG GTG GGC Gly Gln Leu Pro Pro Leu Pro Trp Ala Ser Pro Thr Pro Ser Arg Pro Val Gly	* GGG CAG CTG CCG CCG CTG CCC TGG GCG TCG CCA ACC CCG TCG CGA CCG GTG GGC Gly Gln Leu Pro Pro Leu Pro Trp Ala Ser Pro Thr Pro Ser Arg Pro Val Gly	* GGG CAG CTG CCG CCG CTG CCC TGG GCG TCG CCA ACC CCG TCG CGA CCG GTG GGC Gly Gln Leu Pro Pro Leu Pro Trp Ala Ser Pro Thr Pro Ser Arg Pro Val Gly	* GGG CAG CTG CCG CCG CTG CCC TGG GCG TCG CCA ACC CCG TCG CGA CCG GTG GGC Gly Gln Leu Pro Pro Leu Pro Trp Ala Ser Pro Thr Pro Ser Arg Pro Val Gly	* GGG CAG CTG CCG CCG CTG CCC TGG GCG TCG CCA ACC CCG TCG CGA CCG GTG GGC Gly Gln Leu Pro Pro Leu Pro Trp Ala Ser Pro Thr Pro Ser Arg Pro Val Gly
2140	2150	2160	2170	2180
* CTG CTG CTG TGG TGG GAG CCC TTC GGG GGC GGC GAT AGC GCC CCG AGG CCG CCC Val Leu Leu Trp Trp Trp Glu Pro Phe Gly Gly Arg Asp Ser Ala Pro Arg Pro Pro	* CTG CTG CTG TGG TGG GAG CCC TTC GGG GGC GGC GAT AGC GCC CCG AGG CCG CCC Val Leu Leu Trp Trp Trp Glu Pro Phe Gly Gly Arg Asp Ser Ala Pro Arg Pro Pro	* CTG CTG CTG TGG TGG GAG CCC TTC GGG GGC GGC GAT AGC GCC CCG AGG CCG CCC Val Leu Leu Trp Trp Trp Glu Pro Phe Gly Gly Arg Asp Ser Ala Pro Arg Pro Pro	* CTG CTG CTG TGG TGG GAG CCC TTC GGG GGC GGC GAT AGC GCC CCG AGG CCG CCC Val Leu Leu Trp Trp Trp Glu Pro Phe Gly Gly Arg Asp Ser Ala Pro Arg Pro Pro	* CTG CTG CTG TGG TGG GAG CCC TTC GGG GGC GGC GAT AGC GCC CCG AGG CCG CCC Val Leu Leu Trp Trp Trp Glu Pro Phe Gly Gly Arg Asp Ser Ala Pro Arg Pro Pro
2200	2210	2220	2230	2240
* CCT GAC TGC CCG CTG CCG TTC AAC ATC AGC GGC TGC CCG CTG CTC ACC GAC GCG Pro Asp Cys Pro Leu Arg Phe Asn Ile Ser Gly Cys Arg Leu Thr Thr Asp Arg	* CCT GAC TGC CCG CTG CCG TTC AAC ATC AGC GGC TGC CCG CTG CTC ACC GAC GCG Pro Asp Cys Pro Leu Arg Phe Asn Ile Ser Gly Cys Arg Leu Thr Thr Asp Arg	* CCT GAC TGC CCG CTG CCG TTC AAC ATC AGC GGC TGC CCG CTG CTC ACC GAC GCG Pro Asp Cys Pro Leu Arg Phe Asn Ile Ser Gly Cys Arg Leu Thr Thr Asp Arg	* CCT GAC TGC CCG CTG CCG TTC AAC ATC AGC GGC TGC CCG CTG CTC ACC GAC GCG Pro Asp Cys Pro Leu Arg Phe Asn Ile Ser Gly Cys Arg Leu Thr Thr Asp Arg	* CCT GAC TGC CCG CTG CCG TTC AAC ATC AGC GGC TGC CCG CTG CTC ACC GAC GCG Pro Asp Cys Pro Leu Arg Phe Asn Ile Ser Gly Cys Arg Leu Thr Thr Asp Arg
2250	2260	2270	2280	2290
* GCG TCC TAC GGA GAG GCT CAG GCC GTG CTT TTC CAC CGC GAC CTC GTG AAG Ala Ser Tyr Gly Glu Ala Ala Ala Val Leu Phe His Arg Asp Leu Val Lys	* GCG TCC TAC GGA GAG GCT CAG GCC GTG CTT TTC CAC CGC GAC CTC GTG AAG Ala Ser Tyr Gly Glu Ala Ala Ala Val Leu Phe His Arg Asp Leu Val Lys	* GCG TCC TAC GGA GAG GCT CAG GCC GTG CTT TTC CAC CGC GAC CTC GTG AAG Ala Ser Tyr Gly Glu Ala Ala Ala Val Leu Phe His Arg Asp Leu Val Lys	* GCG TCC TAC GGA GAG GCT CAG GCC GTG CTT TTC CAC CGC GAC CTC GTG AAG Ala Ser Tyr Gly Glu Ala Ala Ala Val Leu Phe His Arg Asp Leu Val Lys	* GCG TCC TAC GGA GAG GCT CAG GCC GTG CTT TTC CAC CGC GAC CTC GTG AAG Ala Ser Tyr Gly Glu Ala Ala Ala Val Leu Phe His Arg Asp Leu Val Lys

FIG. 4F

2300 *	2310 *	2320 *	2330 *	2340 *	2350 *
GGG CCC CCC GAC TGG CCC CCG CCC TGG GGC ATC CAG GCG CAC ACT GCC GAG GAG					
Gly Pro Pro Asp Trp Pro Pro Pro Trp Gly Ile Gln Ala His Thr Ala Glu Glu					
2360 *	2370 *	2380 *	2390 *	2400 *	
GTG GAT CTG CGC GTG TTG GAC TAC GAG GAG GCA GCG GCG GCG GAA GCC CTG					
Val Asp Leu Arg Val Leu Asp Tyr Glu Glu Ala Ala Ala Glu Ala Leu					
2410 *	2420 *	2430 *	2440 *	2450 *	2460 *
GCG ACC TCC AGC CCC AGG CCC CCG GGC CAG CGC TGG GTT TGG ATG AAC TTC GAG					
Ala Thr Ser Ser Pro Arg Pro Arg Pro Gly Gln Arg Trp Val Trp Met Asn Phe Gln					
2470 *	2480 *	2490 *	2500 *	2510 *	
TCG CCC TCG CAC TCC CCG GGC GAC TCG GAC TCG TTT GTG CCT TAT GGC TAC CTC TAC					
Ser Pro Ser His ser Pro Gly Leu Arg Ser Leu Ala Ser Asn Leu Phe Asn Trp					
2520 *	2530 *	2540 *	2550 *	2560 *	
ACG CTC TCC TAC CCG GCG GAC TCG GAC TCG TTT GTG CCT TAT GGC TAC CTC TAC					
Thr Leu Ser Tyr Arg Ala Asp Ser Asp Val Phe Val Pro Tyr Gly Tyr Leu Tyr					
2570 *	2580 *	2590 *	2600 *	2610 *	2620 *
CCC AGA AGC CAC CCC GGC GAC CCG CCC TCA GGC CTG GCC CCG CCA CTG TCC AGG					
Pro Arg Ser His Pro Gly Asp Pro Pro Ser Gly Leu Ala Pro Pro Leu Ser Arg					
2630 *	2640 *	2650 *	2660 *	2670 *	
AAA CAG GGG CTG GTG GCA TGG GTG GTG AGC CAC TGG GAC GAG CGC CAG GCC CGG					
Lys Gln Gly Leu Val Ala Trp Val Val Ser His Trp Asp Glu Arg Gln Ala Arg					

FIG. 46

2680	2690	2700	2710	2720	2730
* GTC CGC TAC TAC CAC CAA CTG AGC CAA CAT GTG ACC GTG GAC GTG TTC GGC CGG	* Val Arg Tyr Tyr His Gln Leu Ser Gln His Val Thr Val Asp Val Phe Gly Arg	*	*	*	*
2740	2750	2760	2770	2780	
* CGC GGC CCC GGC CAG CCG GTG CCC GAA ATT GGG CTC CTG CAC ACA GTG GCC CGC	* Gly Gly Pro Gly Gln Pro Val Pro Gln Ile Gly Leu Leu His Thr Val Ala Arg	*	*	*	
2790	2800	2810	2820	2830	
* TAC AAG TTC TAC CTG GCT TTC GAG AAC TCG CAG CAC CTG GAT TAT ATC ACC GAG	* Tyr Lys Phe Tyr Leu Ala Phe Gln Asn Ser Gln His Leu Asp Tyr Ile Thr Glu	*	*	*	
2840	2850	2860	2870	2880	2890
* AAG CTC TGG CGC AAC GCG TTG CTC GCT GGT GCG GCG GTG CCG GTG GTG CTG GGC CCA	* Lys Leu Trp Arg Asn Ala Leu Leu Ala Gly Ala Val Pro Val Val Leu Gly Pro	*	*	*	*
2900	2910	2920	2930	2940	
* GAC CGT GCC AAC TAC GAG CCG TTT GTG CCC CGC GCG GCG GCC TTC ATC CAC GTG GAC	* Asp Arg Ala Asn Tyr Glu Arg Phe Val Pro Arg Gly Ala Phe Ile His Val Asp	*	*	*	
2950	2960	2970	2980	2990	3000
* GAC TTC CCA AGT GCC TCC TCC CTG GCC TCG TAC CTG CTT TTC CTC GAC CGC AAC	* Asp Phe Pro Ser Ala Ser Ser Ser Leu Ala Ser Tyr Tyr Leu Phe Leu Asp Arg Asn	*	*	*	*
3010	3020	3030	3040	3050	
* CCC GCG GTC TAT CGC CGC TAC TTC CAC TGG CGC CGG AGC TAC GCT GTC CAC ATC	* Pro Ala Val Tyr Arg Arg Tyr Phe His Trp Arg Ser Tyr Ala Val His Ile	*	*	*	

FIG. 4H

3060	3070	3080	3090	3100
* ACC TCC TTC TGG GAC GAG CCT TGG TGC CGG GTG TGC CAG GCT GTA CAG AGG GCT		*	*	*
Thr Ser Phe Trp Asp Glu Pro Trp Cys Arg Val Cys Gln Ala Val Gln Arg Ala				
3110	3120	3130	3140	3150
* GGG GAC CGG CCC AAG AGC ATA CGG AAC TTG GCC AGC TGG TTC GAG CGG TGA A	*	*	*	*
Gly Asp Arg Pro Lys Ser Ile Arg Asn Leu Ala Ser Trp Phe Glu Arg ***				
3170	3180	3190	3200	3210
* GCCGC GCTCC CCTGG AAGCG ACCCA GGGGA GGCCA AGTTG TCAGC TTTT GATCC TCTAC	*	*	*	*
3230	3240	3250	3260	3270
* TGTGC ATCTC CTGGA CGGCC GCATC ATGGG AGTAA GTTCT TCAAA CACCC ATTTT TGCTC	*	*	*	*
3290	3300	3310	3320	3330
* TATGG GAAAA AAACG ATTTA CCAAT TAATA TTACT CAGCA CAGAG ATGGG GGCCC GGTTT	*	*	*	*
3350	3360	3370	3380	3390
* CCATA TTTT TGCAC AGCTA GCAAT TGGGC TCCCT TTGCT GCTGA TGGGC ATCAT TGTTT	*	*	*	*
3410	3420	3430	3440	3450
* AGGGG TGAAG GAGGG GTTTC TTCCT CACCT TGTA CCAGT GCAGA AATGA AATAG CTTAG	*	*	*	*
3470	3480	3490	3500	3510
* CGGCA AGAAG CCGTT GAGGC GGTTT CCTGA ATTTC CCCAT CTGCC ACAGG CCATA TTGT	*	*	*	*
3520				

3530	3540	3550	3560	3570	3580
* GTGCA	* CAAAT	* ACACA	* TCCCG	* CGTTT	* GACCA
GGCCC	GCTTC	CTCAT	ACTGT	ATTCA	TTCTG
3590	3600	3610	3620	3630	3640
* AAGCA	* GTGGT	* AAGGA	* GTTGG	* AGTGG	* CTGTG
AGGTG	AATT	TGTAG	GCCTT	TGGAG	AAGGA
GCTGC	AG				

FIG. 4I

pFT-3 DNA	ATGGGGCACCGTGGGGCTCGCCGACGGCGGGCGGGCGGGCGGGGTG
pFT-3 AA	1 M G A P W G S P T A A A G G R R G W18
Lewis AA	1 M D . P L G . . . A A K P Q W P W13
pFT-3 DNA	GCGCCGAGCGGGGGCTGCGCATGGACCGTGTGTGCTGGGGCC-----
pFT-3 AA	19 R R G R G L P W T V C V L A A . . 33
Lewis AA	14 R R . . . . . C . L A A L L 22
pFT-3 DNA	--GCCCGGCTTGACGTGTACGGCGGATCACCTAC-----GCT
pFT-3 AA	34. A G L T C T A L I T Y . . A 45
Lewis AA	23F Q L L V A V C F F S Y L R V 36
pFT-3 DNA	TGCTGGGGCAGCTGCCGCGCTGCCCTGGGCG-----TCGCCA-----
pFT-3 AA	46 C W G Q L P P L P W A . . . S P . .58
Lewis AA	37 S R D D A T G S P R A P S G S S R Q54
pFT-3 DNA	-----ACCCCGTCGCGACCG---GTGGGCGTGTGTGTGG---TGGGAGC
pFT-3 AA	59 . . T P S R P . V G V L L W . W E 71
Lewis AA	55 D T T P T R P T L L I L L W T W . 70
pFT-3 DNA	CCTTCGGGGGCGGATAGCGCCCCGAGCGCCCCCTGACTGC
pFT-3 AA	72P F G G R D S A P R P P P D C 86
Lewis AA	71P F H I P V A L S R C . . S 82

FIG. 5A

pFT-3 DNA	CCGCTGGGCTTCAACATCAGCGGCTGCCGCTGCTCACCGACCGCGCTCCTA	
pFT-3 AA	87 P L R F N I S G C R L L T D R A S Y104	
Lewis AA	83 E M V P G T A D C H I T A D R K V Y100	
pFT-3 DNA	CGGAGAGGCTCAGGCCGCTTTTCCACCACCGGACCTCGTGAAGGGCCCC	
pFT-3 AA	105 G E A Q A V L F H H R D L V K G P 121	
Lewis AA	101 P Q A D T V I V H H W D I M S N P 117	
pFT-3 DNA	CCGACTGGCCCCCGCCCTGGGGCATCCAGGCGCACACTGCCGAG	
pFT-3 AA	122P D W P P P P W G I Q A H T A E 136	
Lewis AA	118K S R L P P . . . . . 123	
pFT-3 DNA	GAGGTGGATCTGCGCGTGTGGACTACGAGGAGGCGGCGGCGCAGAAGC	
pFT-3 AA	137 E V D L R V L D Y E E A A A A E A154	
Lewis AA	124 . . . . . 124	
pFT-3 DNA	CCTGGCGACCTCCAGCCCCAGCCCCCGGCCAGCGCTGGGTTGGATGAAC	
pFT-3 AA	155 L A T S S P R P P P G Q R W V W M N 171	
Lewis AA	124 . . . . . 136	
pFT-3 DNA	TCGAGTCGCCCTCGCACTCCCCGGGGCTGCGAAGCCTGGCAAGT	
pFT-3 AA	172F E S P S H S P G L R S L A S 186	
Lewis AA	137L E P P P N C Q H L E A L D . 150	

FIG.5B

pFT-3 DNA	AACCTCTTCAACTGGACGCTCTCTTACCGGGCGGACTCGGACGCTTTGTGCC
pFT-3 AA	187 N L F N W T L S Y R A D S D V F V P204
Lewis AA	151 R Y F N L T M S Y R S D S D I F T P168
pFT-3 DNA	TTATGGCTACCTTACCCAGAAAGC---CACCCGGCGACCCGCTCAGGCC
pFT-3 AA	205 Y G Y L Y P R S . H P G D P P S G 220
Lewis AA	169 Y G W L E P W S G Q P A H P P . 183
pFT-3 DNA	TGGCCCCGCACTGTCCAGGAACAGGGGCTGGTGGCATGGGTG
pFT-3 AA	221L A P P L S R K Q G L V A W V 235
Lewis AA	184L N . . L S A K T E L V A W A 196
pFT-3 DNA	GTGAGCCACTGGACGAGCCAGGCCGGGTCCGCTACTACCACCACTGAG
pFT-3 AA	236 V S H W D E R Q A R V R Y Y H Q L S253
Lewis AA	197 V S N W K P D S A R V R Y Y Q S L Q214
pFT-3 DNA	CCAACATGTGACCGTGGACGTTCTCGGCCGGGGCGGGCGGCGCGGTGC
pFT-3 AA	254 Q H V T V D V F G R G G P G Q P V 270
Lewis AA	215 A H L K V D V Y G R S . . H K P L 229
pFT-3 DNA	CCGAAATTGGCTCTGCACACAGTGGCCCGCTACAAGTTCTAC
pFT-3 AA	271P E I G L L H T V A R Y K F Y 285
Lewis AA	230P K G T M M E T L S R Y K F Y 244

FIG.5C



pFT-3 DNA	CTGGCTTTCGAGAACTCGCAGCACCTGGATTATATACCGAGAAAGCTCTGGCG	
pFT-3 AA	286 L A F E N S Q H L D Y I T E K L W R303	
Lewis AA	245 L A F E N S L H P D Y I T E K L W R262	
pFT-3 DNA	CAACGCGTTGCTCGCTGGGGCGGTGCCGGTGGTGGTGGCCAGACCGTGCCA	
pFT-3 AA	304 N A L L A G A V P V V L G P D R A 320	
Lewis AA	263 N A L E A W A V P V V L G P S R S 279	
pFT-3 DNA	ACTACGAGCGCTTTGTGCCCGCGCGCTTCATCCACGTGGAC	
pFT-3 AA	321N Y E R F V P R G A F I H V D 335	
Lewis AA	280N Y E R F L P P D A F I H V D 294	
pFT-3 DNA	GACTTCCCAAGTGCCTCCTCCCTGGCCCTCGTACCTGCTTTTCCTCGACCGCAA	
pFT-3 AA	336 D F P S A S S L A S Y L L F L D R N353	
Lewis AA	295 D F Q S P K D L A R Y L Q E L D K D312	
pFT-3 DNA	CCCCGCGGTCTATCGCCGCTACTTCCACTGGCGC-----CGGA	
pFT-3 AA	354 P A V Y R R Y F H W R . . . R 365	
Lewis AA	313 H A R Y L S Y F R W R E T L R P R 329	
pFT-3 DNA	GCTACGCTGTCCACATCACCTCCTTC---TGGACGAGCCTTGG	
pFT-3 AA	366S Y A V H I T S F . W D E P W 379	
Lewis AA	330S F . . . . S W A L D . . F 337	

FIG.5D

pFT-3 DNA	TGCCGGGTGTGCCAGGCTGTACAGAGGGCTGGGGACCGGCCCAAGAGCATACG	
pFT-3 AA	380 C R V C Q A V Q R A G D R P K S I R397	
Lewis AA	338 C K A C W K L Q Q E S . R Y Q T V R354	
pFT-3 DNA	GAACTTGGCCAGCTGGTTCGAGCGGTGA	
pFT-3 AA	398 N L A S W F E R 405	
Lewis AA	355 S I A A W F T . 361	

FIG.5E

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## Sequence VI

-120 TTTATGACAAGCTGTGTCTATAAATTATAACAGCTTCTCTCAGGACACTGTGGCCAGGAAG

-60 TGGGTGATCTTCCTTAATGACCCCTCACTCCTCTCTCCTCTCTTCCCAGCTACTCTGACCC

1 M D P L G P A K P Q W L W R R C L A G L  
ATGGATCCCCTGGGCCAGCCACAGTGGCTGTGGCCGCTGTCTGGCCGGGCTG  
ATGGATCCCCTGGTGAGCCAGCCACAATGGCCATGGCCGCTGTCTGGCCGCACTG

61 L F Q L L V A V C F F S Y L R V S R D D  
CTGTTTCAGCTGCTGGTGGCTGTGTTTCTCTCTACCTGCGTGTGTCCCGAGACGAT  
CTATTTTCAGCTGCTGGTGGCTGTGTTTCTCTCTACCTGCGTGTGTCCCGAGACGAT

121 A T G S P R P G L M A V E P V T G A P N  
GCCACTGGATCCCCCTAGGCCAGGCTTATGTCAGTGGAACTGTACCGGGCTCCCAAT  
GCCACTGGATCCCCCTAGG-----GCTCCAGT S

181 G S R C Q D S M A T P A H P T L L I L L  
GGTCCCGCTGCCAGACAGCATGGCGACCCCTGCCACCCCACTGATCCTGCTG  
GGTCCCTCCGACAGGACACC-----ACTCCACCGCGCCCACTCCTGATCCTGCTA  
S R T R

**FIG. 6A**

W T W P F N T P V A L P R C S E M V P G  
 241 TGGACGTGGCCTTTTAAACACACCCGTGGTCTGCCCGCTGCTCAGAGATGGTGCCCGGC  
 TGGACATGGCCTTTCCACATCCCTGTGGTCTGTGCCCGCTGTTTCAGAGATGGTGCCCGGC  
 H I S

A A D C N I T A D S S V Y P Q A D A V I  
 301 GCGCCGACTGCAACATCACTGCCGACTCCAGTGTGTACCCACAGGACGCGGTCTATC  
 ACAGCCGACTGCCACATCACTGCCGACCGCAAGGTGTACCCACAGGACGACACGGTCTATC  
 T H K T

V H H W D I M Y N P S A N L P P P T R P  
 361 GTGCACCACTGGGATATCATGTACAACCCAGTGCCAACTCCCGCCCCACAGGCCG  
 GTGCACCACTGGGATATCATGTCCAACCCCTAAGTACGCTCCACCTTCCCCGAGGCCG  
 S K S R S P

Q G Q R W I W F S M E S P S N C R H L E  
 421 CAGGGCAGCGCTGGATCTGGTTTCAGCATGGAGTCCCCCAGCAACTGCCGGCACCTGGAA  
 CAGGGCAGCGCTGGATCTGGTTCAACTTGGAGCCACCCCTAACTGCCAGCACCTGGAA  
 N L P P Q

A L D G Y F N L T M S Y R S D S D I F T  
 481 GCCCTGGACGGATACTTCAATCTCACCATGTCTACCGCAGGACTCCGACATCTTCACG  
 GCCCTGGACAGATACTTCAATCTCACCATGTCTACCGCAGGACTCCGACATCTTCACG  
 R

P Y G W L E P W S G Q P A H P P L N L S  
 541 CCCTACGGCTGGAGCCGTGGTCCGGCCAGCCTGCCACCCACCGCTCAACCTCTCG  
 CCCTACGGCTGGAGCCGTGGTCCGGCCAGCCTGCCACCCACCGCTCAACCTCTCG

FIG. 6B

601 A K T E L V A W A V S N W K P D S A R V  
 GCCAAGACOGAGCTGGTGGCTGGCGGTGTCCAACTGGAAGCCGGACTCGGCCAGGGTG  
 GCCAAGACOGAGCTGGTGGCTGGCGGTGTCCAACTGGAAGCCGGACTCGGCCAGGGTG

661 R Y Y Q S L Q A H L K V D V Y G R S H K  
 CGCTACTACGAGCCTGCAGGCTCATCTCAAGGTGGACGTGTACGGACGCTCCACAAG  
 CGCTACTACGAGCCTGCAGGCTCATCTCAAGGTGGACGTGTACGGACGCTCCACAAG

721 P L P K G T M M E T L S R Y K F Y L A F  
 CCCCTGCCCAAGGGACCATGATGGAGACGCTGTCCGGTACAAGTTCTATCTGGCCTTC  
 CCCCTGCCCAAGGGACCATGATGGAGACGCTGTCCGGTACAAGTTCTATCTGGCCTTC

781 E N S L H P D Y I T E K L W R N A L E A  
 GAGAACTCCTTGACCCCGACTACATCACCGAAGCTGTGGAGGAACGCCCTGGAGGCC  
 GAGAACTCCTTGACCCCGACTACATCACCGAAGCTGTGGAGGAACGCCCTGGAGGCC

841 W A V P V V L G P S R S N Y E R F L P P  
 TGGGCCGTGCCCGTGGTGGCTGGGCCCCAGCAGAAGCAACTACGAGAGGTTCTTCCGCCCC  
 TGGGCCGTGCCCGTGGTGGCTGGGCCCCAGCAGAAGCAACTACGAGAGGTTCTTCCGCCCC

901 D A F I H V D D F Q S P K D L A R Y L Q  
 GACGCTTCATCCACGTGGATGACTTCCAGAGCCCCAAGGACCTGGCCCCGTACCTGCAG  
 GACGCTTCATCCACGTGGACGACTTCCAGAGCCCCAAGGACCTGGCCCCGTACCTGCAG

961 E L D K D H A R Y L S Y F R W R E T L R  
 GAGCTGGACAAGGACCGCCCGTACCTGAGCTACTTTCGCTGGCGGAGACGCTGCGG  
 GAGCTGGACAAGGACCGCCCGTACCTGAGCTACTTTCGCTGGCGGAGACGCTGCGG

FIG. 6C

P R S F S W A L A F C K A C W K L Q Q E  
1021 CCTCGCTCCTTCAGCTGGGCACTGGCTTCTGCAAGCCCTGCTGGAAGCTGCAGCAGGAA  
CCTCGCTCCTTCAGCTGGGCACTGGATTCTGCAAGCCCTGCTGGAACCTGCAGCAGGAA  
D

S R Y Q T V R S I A A W F T U  
1081 TCCAGGTACCAGACGGTGCGCAGCATAGCGGCTTGTTTACCTGAGAGGCCGCGCATGGGG  
TCCAGGTACCAGACGGTGCGCAGCATAGCGGCTTGTTTACCTGA

1141 CCTGGGCTGCCAGGGACCTCACTTCCCAGGGCCTCACCTACCTAGGTC // TCTAGA

FIG. 6D

$\alpha$ (1,3)FT DNA (-128)	TTTTCTCA
$\alpha$ (1,3)FT DNA (-120)	TCTGTGAACAGGAATAATAACAGCTCTTCTCAGGACTCATGGCCTGGAGCTTTGGTAAG
$\alpha$ (1,3)FT DNA (-60)	CAGGAGATTGTCATCAATGACCCCTCACTCCTCTCTCTCCCACTTCCAGAGACTCTGACCC
$\alpha$ (1,3)FT AA	M D P L G P A K P Q W S W R C C L T T L
$\alpha$ (1,3) DNA (1)	ATGGATCCCCCTGGGCCCCGCAAGCCACAGTGGTGGTGGCGCTGCTGTCTGACCACGCTG
Lewis FT DNA	       ATGGATCCCCCTGGGTGCAGCCCAAGCCACAATGGCCATGGCGCGCTGTCTGGCGCACTG
$\alpha$ (1,3)FT AA	L F Q L L M A V C F F S Y L R V S Q D D
$\alpha$ (1,3)FT DNA (61)	CTGTTTCAGCTGCTGATGGCTGTGTGTTTCTTCTCCTATCTGCGTGTCTCAAGACGAT
	       CTATTTCAGCTGCTGGTGGCTGTGTGTTTCTTCTCCTACCTGCGTGTCTCCGAGACGAT
$\alpha$ (1,3)FT AA	P T V Y P N G S R F P D S T G T P A H S
$\alpha$ (1,3)FT DNA (121)	CCCACTGTGTACCCCTAATGGGTCC...CGCTTCCCA..GACAGCACAGGACCCCGCCCACTCC
Lewis FT DNA	       GCCACTGGATCCCCCTAG.GGCTCCCAGTGGGTCTCTCCGACAGGACACC.ACTCCACCCGCCCC
$\alpha$ (1,3)FT AA	I P L I L L W T W P F N K P I A L P R C
$\alpha$ (1,3)FT DNA (181)	ATCCCCCTGATCCTGCTGTGGACGTGGCCCTTTTAACAAACCCATAGCTCTGCCCGCTGC
Lewis FT DNA	       ACCTCCTGATCCTGCTATGGACATGGCCCTTTCCACATCCCTGTGGCTCTGTCCCGCTGT

FIG. 7A

$\alpha(1,3)$ FT AA  
 $\alpha(1,3)$  FT DNA (241)  
 Lewis FT DNA

S E M V P G T A D C N I T A D R K V Y P  
 TCAGAGATGGTGCCTGGCAGCGGTGACTGCAACATCACTGCCGACCGCAAGGTGTATCCA  
 |||||  
 TCAGAGATGGTGCCTGGCAGCGGTGACTGCAACATCACTGCCGACCGCAAGGTGTATCCA

$\alpha(1,3)$ FT AA  
 $\alpha(1,3)$  FT DNA (301)  
 Lewis FT DNA

Q A D A V I V H H R E V M Y N P S A Q L  
 CAGGCAGACGCGGTCACTGTCACACCGAGAGGTGATGTACAACCCAGTGCCTCAGCTC  
 |||||  
 CAGGCAGACACGCGGTCACTGTCACACCGAGAGGTGATGTACAACCCAGTGCCTCAGCTC

$\alpha(1,3)$ FT AA  
 $\alpha(1,3)$  FT DNA (361)  
 Lewis FT DNA

P R S P R R Q G Q R W I W F S M E S P S  
 CCACGCTCCCCGAGCGCGCAGGGCAGCGATGGATCTGGTTCAGCATGGAGTCCCCAAGC  
 |||||  
 CCACCTTCCCCGAGCGCGCAGGGCAGCGCTGGATCTGGTTCAACTTGGAGCCACCCCT

$\alpha(1,3)$ FT AA  
 $\alpha(1,3)$  FT DNA (421)  
 Lewis FT DNA

H C W Q L K A M D G Y F N L T M S Y R S  
 CACTGCTGGCAGCTGAAGCCATGGACGGATACTTCAATCTCACCATGTCTACCGCAGC  
 |||||  
 AACTGCCAGCACCTGGAAGCCCTGGACAGATACTTCAATCTCACCATGTCTACCGCAGC

$\alpha(1,3)$ FT AA  
 $\alpha(1,3)$  FT DNA (481)  
 Lewis FT DNA

D S D I F T P Y G W L E P W S G Q P A H  
 GACTCCGACATCTTACGCCCTACGGCTGGCTGGAGCCGCTGGTCCGGCCAGCCTGCCAC  
 |||||  
 GACTCCGACATCTTACGCCCTACGGCTGGCTGGAGCCGCTGGTCCGGCCAGCCTGCCAC

FIG. 7B



$\alpha(1,3)$ FT AA	P P L N L S A K T E L V A W A V S N W G
$\alpha(1,3)$ FT DNA (541)	CCACCGCTCAACCTCTCGGCCAAGACCGAGCTGGTGGCTGGCAGTGTCCAACCTGGGGG             CCACCGCTCAACCTCTCGGCCAAGACCGAGCTGGTGGCTGGCAGTGTCCAACCTGGAAG
Lewis FT DNA	

[illegible]

$\alpha(1,3)$ FT AA	Y G R S H K P L P Q G T M E T L S R Y
$\alpha(1,3)$ FT DNA (661)	TACGACGCTCCACAAGCCCTGCCCCAGGAACCATGATGGAGACGCTGTCCCGGTAC
	TACGACGCTCCACAAGCCCTGCCCAAGGGACCATGATGGAGACGCTGTCCCGGTAC
Lewis FT DNA	

$\alpha(1,3)$ FT AA	K F Y L A F E N S L H P D Y I T E K L W
$\alpha(1,3)$ FT DNA (721)	AAGTTCTATCTGGCCTTCGAGAACTCCTTGACCCCGACTACATCACCAGAAAGCTGTGG
	AAGTTCTACCTGGCCTTCGAGAACTCCTTGACCCCGACTACATCACCAGAAAGCTGTGG
Lewis FT DNA	

$\alpha(1,3)$ FT AA	R N A L E A W A V V L G P S R S N Y
$\alpha(1,3)$ FT DNA (781)	AGGAACGCCCTGGAGGCTGGCCCGTGGTGCTGGGCCCCCAGCAGAAGCAACTAC       AGGAACGCCCTGGAGGCTGGCCCGTGGTGCTGGGCCCCCAGCAGAAGCAACTAC
Lewis FT DNA	

FIG. 7C

$\alpha(1,3)$  FT AA  
 $\alpha(1,3)$  FT DNA (841)  
 Lewis FT DNA

E R F L P P D A F I H V D D F Q S P K D  
 GAGAGTTCTGCGCACCCGACGCTTTCATCCAGTGGACGACTTCCAGAGCCCCAAGGAC  
 |||||  
 GAGAGTTCTGCGCACCCGACGCTTTCATCCAGTGGACGACTTCCAGAGCCCCAAGGAC

$\alpha(1,3)$  FT AA  
 $\alpha(1,3)$  FT DNA (901)  
 Lewis FT DNA

L A R Y L Q E L D K D H A R Y L S Y F R  
 CTGGCCCGGTACTGTCAGGAGCTGGACAAGGACCACGCCCGCTACTGAGCTACTTTCGC  
 |||||  
 CTGGCCCGGTACTGTCAGGAGCTGGACAAGGACCACGCCCGCTACTGAGCTACTTTCGC

$\alpha(1,3)$  FT AA  
 $\alpha(1,3)$  FT DNA (961)  
 Lewis FT DNA

W R E T L R P R S F S W A L A F C K A C  
 TGGCGGAGACGCTGCGGCTCGCTCCTTCAGCTGGGCACTCGCTTCTGCAAGGCCTGC  
 |||||  
 TGGCGGAGACGCTGCGGCTCGCTCCTTCAGCTGGGCACTGGATTCTGCAAGGCCTGC

$\alpha(1,3)$  FT AA  
 $\alpha(1,3)$  FT DNA (1021)  
 Lewis FT DNA

W K L Q E E S R Y Q T R G I A A W F T Stop  
 TGGAAACTGCAGGAGGAATCCAGGTACCAGACACGCGGC...ATAGCGGCTTGGTTCACCTGA  
 |||||  
 TGGAAACTGCAGGAGGAATCCAGGTACCAGACGCGGTGCGCAGCATAGCGGCTTGGTTCACCTGA

GAGGCTGGTGGGCTGGGCTGCCAGGAACCTCATTTCTGGGGCTCACCTGAGTG  
 GGGCCCTCATCTACCTAAGGACTCGTTTGCTGAAGCTTCACTGCTGAGGACTCACCT  
 GCTGGACGGTCACTGTTGCAGCTTCACTGCTGGGATTCACCTACCTGGTCCCTC  
 ACTTCTGGGCTCACCTGCTGGAGTCTTGGTGGCCAGGATGTCCTTACCTGGGA  
 TTTACATGCTGGCTTCCAGGAGCGTCCCTGCGGAAGCCTGGCTGCTGGGATGTCTC  
 CTGGGACTTTCCTACTGGGACCTCGGCTGTTGGGACTTACCTGCTGGGACCTGCT  
 CCCAGAGACCTTCCACACTGAATCTCACCTGCTAGGAGCCTCACCTGCTGGGACCTCAC  
 CCTGGAGGCACTGGGCCCTGGGAAT

FIG. 7D

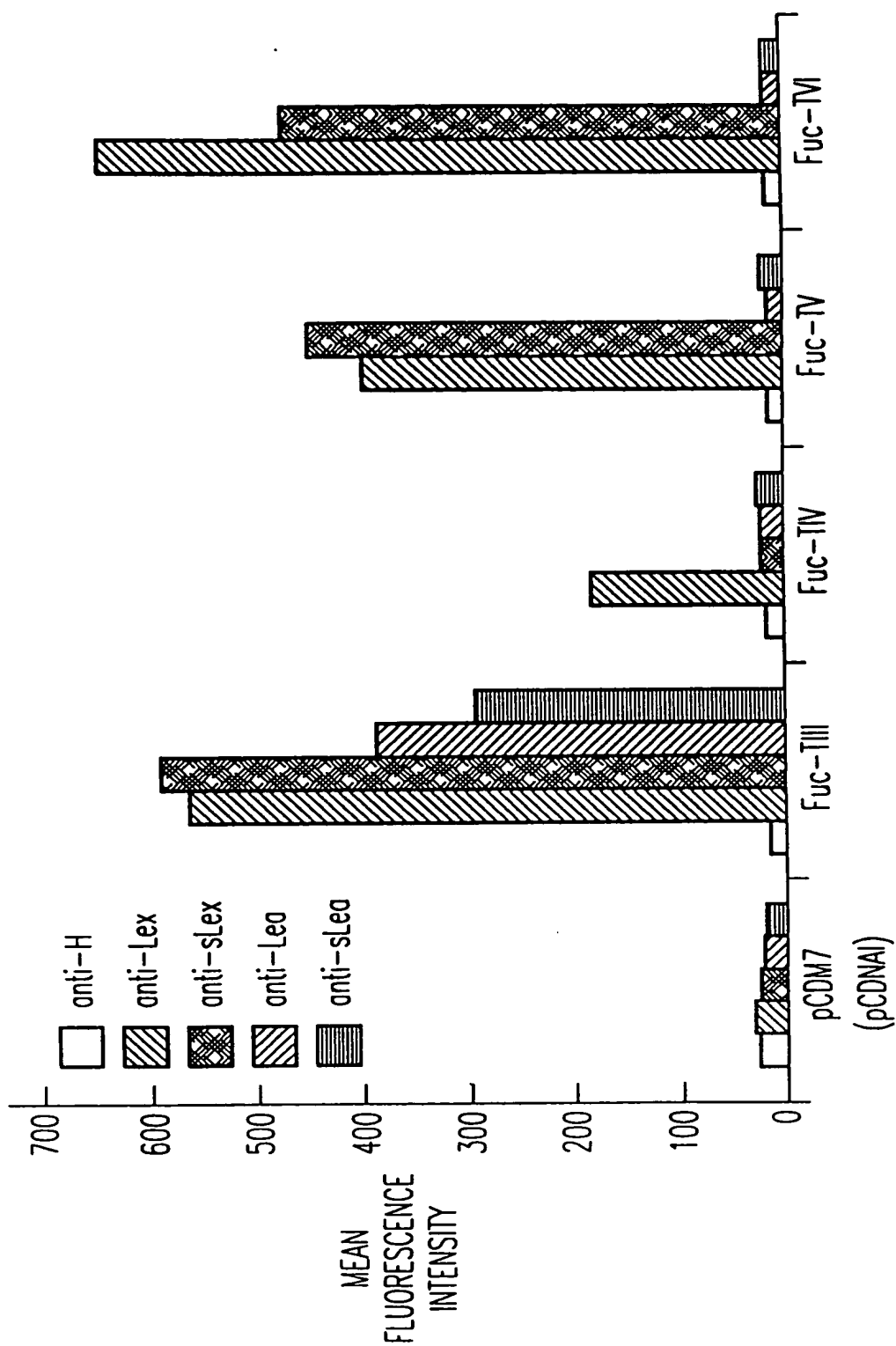


FIG. 8